

1600

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/654,449

DATE: 11/14/2001

TIME: 15:14:55

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AUG 04 2003

TECH CENTER 1600/2900

Input Set : A:\4085-226-27.ST25.txt
 Output Set: N:\CRF3\11142001\I654449.raw

3 <110> APPLICANT: Palmer, Michelle A.J.
 4 Gee, Melissa
 5 Tillotson, Bonnie
 6 Chang, Xiao-Jia
 8 <120> TITLE OF INVENTION: Receptor Function Assay for G-Protein Coupled Receptors and Orphan

Receptors by Reporter Enzyme Mutant Complementation

11 <130> FILE REFERENCE: 4085-226-27
 13 <140> CURRENT APPLICATION NUMBER: US/09/654,449

14 <141> CURRENT FILING DATE: 2000-09-01

16 <150> PRIOR APPLICATION NUMBER: US 60/180,669

17 <151> PRIOR FILING DATE: 2000-02-07

19 <160> NUMBER OF SEQ ID NOS: 5

21 <170> SOFTWARE: FastSEQ for Windows Version 4.0

23 <210> SEQ ID NO: 1

24 <211> LENGTH: 6700

25 <212> TYPE: DNA

26 <213> ORGANISM: Artificial Sequence

28 <220> FEATURE:

29 <223> OTHER INFORMATION: Nucleotide sequence for pICAST ALC ✓

31 <221> NAME/KEY: CDS

32 <222> LOCATION: (1457)...(4486)

34 <400> SEQUENCE: 1

35 ctgcagcctg aatatgggccc aaacaggata tctgtggttaa gcagttcctg ccccggtctca 60
 36 gggccaagaa cagatggaac agctgaatat gggccaaaca ggatatctgt ggtaagcagt 120
 37 tcctgccccg gctcaggggc aagaacagat ggtccccaga tgcggtccag cccctcagcag 180
 38 tttctagaga accatcagat gtttccagggt tgccccaaagg acctgaaatg accctgtgoc 240
 39 ttatttgaac taaccaatca gttcgttctt cgcttctgtt cgcgcgcttc tgetccccga 300
 40 gctcaataaa agagcccaca acccctcact cggggcgcca gtctctcgat tgaactgagtc 360
 41 gcccggttac ccgtgtatcc aataaaccct cttgcagttg catccgactt gtggtctcgc 420
 42 tgttccttgg gaggggtctcc tctgagtgtat tgactaccgc tcagcggggg tctttcattt 480
 43 gggggctcgt ccgggatcgg gagacccttg cccaggggacc accgaccac caccgggagg 540
 44 caagctggcc agcaacttat ctgtgtctgt ccgattgtct agtgtctatg actgatttta 600
 45 tgcgcctgcg tcggtactag ttagctaact agctctgtat ctggcggacc cgtggtggaa 660
 46 ctgacgagtt ctgaacaccc ggccgcaacc ctgggagacg tcccaggggac tttggggggc 720
 47 gtttttgtgg cccgacctga ggaagggagt cgatgtggaa tccgaccccg tcaggatatg 780
 48 tggttctggt aggagacgag aacctaaaac agttcccgc tccgtctgaa tttttgottt 840
 49 cggtttgtaa ccgaagccgc gcgtcttgtc tgetgcagca tcgttctgtg ttgtctctgt 900
 50 ctgactgtgt ttctgtattt gtctgaaaat tagggccaga ctgttaccac tcccttaagt 960
 51 ttgaccttag gtaactggaa agatgtcgag cggctcgtc acaaccagtc ggtagatgtc 1020
 52 aagaagagac gttgggttae etttctgtct gcagaatggc caacctttaa cgtcggatgg 1080
 53 ccgcgagacg gcacctttaa ccgagacctc atcaccagg ttaagatcaa ggtcttttca 1140
 54 cctggccgcg atggacaccc agacaggctc cctacatcg tgacctggga agccttggtc 1200
 55 tttgaccccc ctccctgggt caagcccttt gtacacccta agcctccgcc tctcttctct 1260
 56 ccatccggccc cgtctctccc ccttgaacct cctcgttcga cccgcctcgc atcctccctt 1320
 57 tatccagccc tcaactccttc tctagggccc ggccgctcta gccattaat acgactcaat 1380
 58 atagggcgat tcgaatcagg ccttggcgcg ccggatcctt aattaagcgc aattgggagg 1440
 59 tggcggtagc ctcgag atg ggc gtg att acg gat tca ctg gcc gtc gtg gcc 1492

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60           Met Gly Val Ile Thr Asp Ser Leu Ala Val Val Ala
61           1           5           10
63 cgc acc gat cgc cct tcc caa cag tta cgc agc ctg aat ggc gaa tgg 1540
64 Arg Thr Asp Arg Pro Ser Gln Gln Leu Arg Ser Leu Asn Gly Glu Trp
65           15           20           25
67 cgc ttt gcc tgg ttt ccg gca cca gaa gcg gtg ccg gaa agc tgg ctg 1588
68 Arg Phe Ala Trp Phe Pro Ala Pro Glu Ala Val Pro Glu Ser Trp Leu
69           30           35           40
71 gag tgc gat ctt cct gag gcc gat act gtc gtc gtc ccc tca aac tgg 1636
72 Glu Cys Asp Leu Pro Glu Ala Asp Thr Val Val Val Pro Ser Asn Trp
73 45           50           55           60
75 cag atg cac ggt tac gat gcg ccc atc tac acc aac gtg acc tat ccc 1684
76 Gln Met His Gly Tyr Asp Ala Pro Ile Tyr Thr Asn Val Thr Tyr Pro
77           65           70           75
79 att acg gtc aat ccg ccg ttt gtt ccc acg gag aat ccg acg ggt tgt 1732
80 Ile Thr Val Asn Pro Pro Phe Val Pro Thr Glu Asn Pro Thr Gly Cys
81           80           85           90
83 tac tcg ctc aca ttt aat gtt gat gaa agc tgg cta cag gaa ggc cag 1780
84 Tyr Ser Leu Thr Phe Asn Val Asp Glu Ser Trp Leu Gln Glu Gly Gln
85           95           100           105
87 acg cga att att ttt gat ggc gtt aac tcg gcg ttt cat ctg tgg tgc 1828
88 Thr Arg Ile Ile Phe Asp Gly Val Asn Ser Ala Phe His Leu Trp Cys
89           110           115           120
91 aac ggg cgc tgg gtc ggt tac ggc cag gac agt cgt ttg ccg tct gaa 1876
92 Asn Gly Arg Trp Val Gly Tyr Gly Gln Asp Ser Arg Leu Pro Ser Glu
93 125           130           135           140
95 ttt gac ctg agc gca ttt tta cgc gcc gga gaa aac cgc ctc gcg gtg 1924
96 Phe Asp Leu Ser Ala Phe Leu Arg Ala Gly Glu Asn Arg Leu Ala Val
97           145           150           155
99 atg gtg ctg cgc tgg agt gac ggc agt tat ctg gaa gat cag gat atg 1972
100 Met Val Leu Arg Trp Ser Asp Gly Ser Tyr Leu Glu Asp Gln Asp Met
101           160           165           170
103 tgg cgg atg agc ggc att ttc cgt gac gtc tcg ttg ctg cat aaa ccg 2020
104 Trp Arg Met Ser Gly Ile Phe Arg Asp Val Ser Leu Leu His Lys Pro
105           175           180           185
107 act aca caa atc agc gat ttc cat gtt gcc act cgc ttt aat gat gat 2068
108 Thr Thr Gln Ile Ser Asp Phe His Val Ala Thr Arg Phe Asn Asp Asp
109           190           195           200
111 ttc agc cgc gct gta ctg gag gct gaa gtt cag atg tgc ggc gag ttg 2116
112 Phe Ser Arg Ala Val Leu Glu Ala Glu Val Gln Met Cys Gly Glu Leu
113 205           210           215           220
115 cgt gac tac cta ccg gta aca gtt tct tta tgg cag ggt gaa acg cag 2164
116 Arg Asp Tyr Leu Arg Val Thr Val Ser Leu Trp Gln Gly Glu Thr Gln
117           225           230           235
119 gtc gcc agc ggc acc gcg cct ttc ggc ggt gaa att atc gat gag cgt 2212
120 Val Ala Ser Gly Thr Ala Pro Phe Gly Gly Glu Ile Ile Asp Glu Arg
121           240           245           250
123 ggt ggt tat gcc gat cgc gtc aca cta cgt ctg aac gtc gaa aac ccg 2260
124 Gly Gly Tyr Ala Asp Arg Val Thr Leu Arg Leu Asn Val Glu Asn Pro

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| | | | | |
|-----|---|------|-----|--|
| 125 | 255 | 260 | 265 | |
| 127 | aaa ctg tgg agc gcc gaa atc ccg aat ctc tat cgt gcg gtg gtt gaa | 2308 | | |
| 128 | Lys Leu Trp Ser Ala Glu Ile Pro Asn Leu Tyr Arg Ala Val Val Glu | | | |
| 129 | 270 275 280 | | | |
| 131 | ctg cac acc gcc gac ggc acg ctg att gaa gca gaa gcc tgc gat gtc | 2356 | | |
| 132 | Leu His Thr Ala Asp Gly Thr Leu Ile Glu Ala Glu Ala Cys Asp Val | | | |
| 133 | 285 290 295 300 | | | |
| 135 | ggt ttc cgc gag gtg cgg att gaa aat ggt ctg ctg ctg ctg aac ggc | 2404 | | |
| 136 | Gly Phe Arg Glu Val Arg Ile Glu Asn Gly Leu Leu Leu Leu Asn Gly | | | |
| 137 | 305 310 315 | | | |
| 139 | aag ccg ttg ctg att cga ggc gtt aac cgt cac gag cat cat cct ctg | 2452 | | |
| 140 | Lys Pro Leu Leu Ile Arg Gly Val Asn Arg His Glu His His Pro Leu | | | |
| 141 | 320 325 330 | | | |
| 143 | cat ggt cag gtc atg gat gag cag acg atg gtg cag gat atc ctg ctg | 2500 | | |
| 144 | His Gly Gln Val Met Asp Glu Gln Thr Met Val Gln Asp Ile Leu Leu | | | |
| 145 | 335 340 345 | | | |
| 147 | atg aag cag aac aac ttt aac gcc gtg cgc tgt tcg cat tat ccg aac | 2548 | | |
| 148 | Met Lys Gln Asn Asn Phe Asn Ala Val Arg Cys Ser His Tyr Pro Asn | | | |
| 149 | 350 355 360 | | | |
| 151 | cat ccg ctg tgg tac acg ctg tgc gac cgc tac ggc ctg tat gtg gtg | 2596 | | |
| 152 | His Pro Leu Trp Tyr Thr Leu Cys Asp Arg Tyr Gly Leu Tyr Val Val | | | |
| 153 | 365 370 375 380 | | | |
| 155 | gat gaa gcc aat att gaa acc cac ggc atg gtg cca atg aat cgt ctg | 2644 | | |
| 156 | Asp Glu Ala Asn Ile Glu Thr His Gly Met Val Pro Met Asn Arg Leu | | | |
| 157 | 385 390 395 | | | |
| 159 | acc gat gat ccg cgc tgg cta ccg gcg atg agc gaa cgc gta acg cga | 2692 | | |
| 160 | Thr Asp Asp Pro Arg Trp Leu Pro Ala Met Ser Glu Arg Val Thr Arg | | | |
| 161 | 400 405 410 | | | |
| 163 | atg gtg cag cgc gat cgt aat cac ccg agt gtg atc atc tgg tcg ctg | 2740 | | |
| 164 | Met Val Gln Arg Asp Arg Asn His Pro Ser Val Ile Ile Trp Ser Leu | | | |
| 165 | 415 420 425 | | | |
| 167 | ggg aat gaa tca ggc cac ggc gct aat cac gac gcg ctg tat cgc tgg | 2788 | | |
| 168 | Gly Asn Glu Ser Gly His Gly Ala Asn His Asp Ala Leu Tyr Arg Trp | | | |
| 169 | 430 435 440 | | | |
| 171 | atc aaa tct gtc gat cct tcc cgc ccg gtg cag tat gaa ggc ggc gga | 2836 | | |
| 172 | Ile Lys Ser Val Asp Pro Ser Arg Pro Val Gln Tyr Glu Gly Gly Gly | | | |
| 173 | 445 450 455 460 | | | |
| 175 | gcc gac acc acg gcc acc gat att att tgc ccg atg tac gcg cgc gtg | 2884 | | |
| 176 | Ala Asp Thr Thr Ala Thr Asp Ile Ile Cys Pro Met Tyr Ala Arg Val | | | |
| 177 | 465 470 475 | | | |
| 179 | gat gaa gac cag ccc ttc ccg gct gtg ccg aaa tgg tcc atc aaa aaa | 2932 | | |
| 180 | Asp Glu Asp Gln Pro Phe Pro Ala Val Pro Lys Trp Ser Ile Lys Lys | | | |
| 181 | 480 485 490 | | | |
| 183 | tgg ctt tcg cta cct gga gag acg cgc ccg ctg atc ctt tgc gaa tac | 2980 | | |
| 184 | Trp Leu Ser Leu Pro Gly Glu Thr Arg Pro Leu Ile Leu Cys Glu Tyr | | | |
| 185 | 495 500 505 | | | |
| 187 | gcc cac gcg atg ggt aac agt ctt ggc ggt ttc gct aaa tac tgg cag | 3028 | | |
| 188 | Ala His Ala Met Gly Asn Ser Leu Gly Gly Phe Ala Lys Tyr Trp Gln | | | |
| 189 | 510 515 520 | | | |

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| 191 | gcg | ttt | cgt | cag | tat | ccc | cgt | tta | cag | ggc | ggc | ttc | gtc | tgg | gac | tgg | 3076 |
| 192 | Ala | Phe | Arg | Gln | Tyr | Pro | Arg | Leu | Gln | Gly | Gly | Phe | Val | Trp | Asp | Trp | |
| 193 | 525 | | | | | 530 | | | | | | 535 | | | | 540 | |
| 195 | gtg | gat | cag | tgc | ctg | att | aaa | tat | gat | gaa | aac | ggc | aac | ccg | tgg | tgc | 3124 |
| 196 | Val | Asp | Gln | Ser | Leu | Ile | Lys | Tyr | Asp | Glu | Asn | Gly | Asn | Pro | Trp | Ser | |
| 197 | | | | | | 545 | | | | | | 550 | | | | 555 | |
| 199 | gct | tac | ggc | ggt | gat | ttt | ggc | gat | acg | ccg | aac | gat | cgc | cag | ttc | tgt | 3172 |
| 200 | Ala | Tyr | Gly | Gly | Asp | Phe | Gly | Asp | Thr | Pro | Asn | Asp | Arg | Gln | Phe | Cys | |
| 201 | | | | | | 560 | | | | | | 565 | | | | 570 | |
| 203 | atg | aac | ggt | ctg | gtc | ttt | gcc | gac | cgc | acg | ccg | cat | cca | gcg | ctg | acg | 3220 |
| 204 | Met | Asn | Gly | Leu | Val | Phe | Ala | Asp | Arg | Thr | Pro | His | Pro | Ala | Leu | Thr | |
| 205 | | | | | | 575 | | | | | | 580 | | | | 585 | |
| 207 | gaa | gca | aaa | cac | cag | cag | cag | ttt | ttc | cag | ttc | cgt | tta | tcc | ggg | caa | 3268 |
| 208 | Glu | Ala | Lys | His | Gln | Gln | Gln | Phe | Phe | Gln | Phe | Arg | Leu | Ser | Gly | Gln | |
| 209 | | | | | | 590 | | | | | | 600 | | | | | |
| 211 | acc | atc | gaa | gtg | acc | agc | gaa | tac | ctg | ttc | cgt | cat | agc | gat | aac | gag | 3316 |
| 212 | Thr | Ile | Glu | Val | Thr | Ser | Glu | Tyr | Leu | Phe | Arg | His | Ser | Asp | Asn | Glu | |
| 213 | 605 | | | | | 610 | | | | | | 615 | | | | 620 | |
| 215 | ctc | ctg | cac | tgg | atg | gtg | gcg | ctg | gat | ggt | aag | ccg | ctg | gca | agc | ggt | 3364 |
| 216 | Leu | Leu | His | Trp | Met | Val | Ala | Leu | Asp | Gly | Lys | Pro | Leu | Ala | Ser | Gly | |
| 217 | | | | | | 625 | | | | | | 630 | | | | 635 | |
| 219 | gaa | gtg | cct | ctg | gat | gtc | gct | cca | caa | ggt | aaa | cag | ttg | att | gaa | ctg | 3412 |
| 220 | Glu | Val | Pro | Leu | Asp | Val | Ala | Pro | Gln | Gly | Lys | Gln | Leu | Ile | Glu | Leu | |
| 221 | | | | | | 640 | | | | | | 645 | | | | 650 | |
| 223 | cct | gaa | cta | ccg | cag | ccg | gag | agc | gcc | ggg | caa | ctc | tgg | ctc | aca | gta | 3460 |
| 224 | Pro | Glu | Leu | Pro | Gln | Pro | Glu | Ser | Ala | Gly | Gln | Leu | Trp | Leu | Thr | Val | |
| 225 | | | | | | 655 | | | | | | 660 | | | | 665 | |
| 227 | cgc | gta | gtg | caa | ccg | aac | gcg | acc | gca | tgg | tca | gaa | gcc | ggg | cac | atc | 3508 |
| 228 | Arg | Val | Val | Gln | Pro | Asn | Ala | Thr | Ala | Trp | Ser | Glu | Ala | Gly | His | Ile | |
| 229 | | | | | | 670 | | | | | | 675 | | | | 680 | |
| 231 | agc | gcc | tgg | cag | cag | tgg | cgt | ctg | gcg | gaa | aac | ctc | agt | gtg | acg | ctc | 3556 |
| 232 | Ser | Ala | Trp | Gln | Gln | Trp | Arg | Leu | Ala | Glu | Asn | Leu | Ser | Val | Thr | Leu | |
| 233 | 685 | | | | | 690 | | | | | | 695 | | | | 700 | |
| 235 | ccc | gcc | gcg | tcc | cac | gcc | atc | ccg | cat | ctg | acc | acc | agc | gaa | atg | gat | 3604 |
| 236 | Pro | Ala | Ala | Ser | His | Ala | Ile | Pro | His | Leu | Thr | Thr | Ser | Glu | Met | Asp | |
| 237 | | | | | | 705 | | | | | | 710 | | | | 715 | |
| 239 | ttt | tgc | atc | gag | ctg | ggt | aat | aag | cgt | tgg | caa | ttt | aac | cgc | cag | tca | 3652 |
| 240 | Phe | Cys | Ile | Glu | Leu | Gly | Asn | Lys | Arg | Trp | Gln | Phe | Asn | Arg | Gln | Ser | |
| 241 | | | | | | 720 | | | | | | 725 | | | | 730 | |
| 243 | ggc | ttt | ctt | tca | cag | atg | tgg | att | ggc | gat | aaa | aaa | caa | ctg | ctg | acg | 3700 |
| 244 | Gly | Phe | Leu | Ser | Gln | Met | Trp | Ile | Gly | Asp | Lys | Lys | Gln | Leu | Leu | Thr | |
| 245 | | | | | | 735 | | | | | | 740 | | | | 745 | |
| 247 | ccg | ctg | cgc | gat | cag | ttc | acc | cgt | gca | ccg | ctg | gat | aac | gac | att | ggc | 3748 |
| 248 | Pro | Leu | Arg | Asp | Gln | Phe | Thr | Arg | Ala | Pro | Leu | Asp | Asn | Asp | Ile | Gly | |
| 249 | | | | | | 750 | | | | | | 755 | | | | 760 | |
| 251 | gta | agt | gaa | gcg | acc | cgc | att | gac | eet | aac | gcc | tgg | gtc | gaa | cgc | tgg | 3796 |
| 252 | Val | Ser | Glu | Ala | Thr | Arg | Ile | Asp | Pro | Asn | Ala | Trp | Val | Glu | Arg | Trp | |
| 253 | 765 | | | | | 770 | | | | | | 775 | | | | 780 | |
| 255 | aag | gcg | gcg | ggc | cat | tac | cag | gcc | gaa | gca | gcg | ttg | ttg | cag | tgc | acg | 3844 |

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256 Lys Ala Ala Gly His Tyr Gln Ala Glu Ala Ala Leu Leu Gln Cys Thr
257          785          790          795
259 gca gat aca ctt gct gat gcg gtg ctg att acg acc gct cac gcg tgg 3892
260 Ala Asp Thr Leu Ala Asp Ala Val Leu Ile Thr Thr Ala His Ala Trp
261          800          805          810
263 cag cat cag ggg aaa acc tta ttt atc agc cgg aaa acc tac cgg att 3940
264 Gln His Gln Gly Lys Thr Leu Phe Ile Ser Arg Lys Thr Tyr Arg Ile
265          815          820          825
267 gat ggt agt ggt caa atg gcg att acc gtt gat gtt gaa gtg gcg agc 3988
268 Asp Gly Ser Gly Gln Met Ala Ile Thr Val Asp Val Glu Val Ala Ser
269          830          835          840
271 gat aca ccg cat ccg gcg cgg att ggc ctg aac tgc cag ctg gcg cag 4036
272 Asp Thr Pro His Pro Ala Arg Ile Gly Leu Asn Cys Gln Leu Ala Gln
273 845          850          855          860
275 gta gca gag cgg gta aac tgg ctc gga tta ggg ccg caa gaa aac tat 4084
276 Val Ala Glu Arg Val Asn Trp Leu Gly Leu Gly Pro Gln Glu Asn Tyr
277          865          870          875
279 ccc gac cgc ctt act gcc gcc tgt ttt gac cgc tgg gat ctg cca ttg 4132
280 Pro Asp Arg Leu Thr Ala Ala Cys Phe Asp Arg Trp Asp Leu Pro Leu
281          880          885          890
283 tca gac atg tat acc ccg tac gtc ttc ccg agc gaa aac ggt ctg cgc 4180
284 Ser Asp Met Tyr Thr Pro Tyr Val Phe Pro Ser Glu Asn Gly Leu Arg
285          895          900          905
287 tgc ggg acg cgc gaa ttg aat tat ggc cca cac cag tgg cgc ggc gac 4228
288 Cys Gly Thr Arg Glu Leu Asn Tyr Gly Pro His Gln Trp Arg Gly Asp
289          910          915          920
291 ttc cag ttc aac atc agc cgc tac agt caa cag caa ctg atg gaa acc 4276
292 Phe Gln Phe Asn Ile Ser Arg Tyr Ser Gln Gln Gln Leu Met Glu Thr
293 925          930          935          940
295 agc cat cgc cat ctg ctg cac gcg gaa gaa ggc aca tgg ctg aat atc 4324
296 Ser His Arg His Leu Leu His Ala Glu Glu Gly Thr Trp Leu Asn Ile
297          945          950          955
299 gac ggt ttc cat atg ggg att ggt ggc gac gac tcc tgg agc ccg tca 4372
300 Asp Gly Phe His Met Gly Ile Gly Gly Asp Asp Ser Trp Ser Pro Ser
301          960          965          970
303 gta tcg gcg gaa ttc cag ctg agc gcc ggt cgc tac cat tac cag ttg 4420
304 Val Ser Ala Glu Phe Gln Leu Ser Ala Gly Arg Tyr His Tyr Gln Leu
305          975          980          985
307 gtc tgg tgt caa aaa aga tct gac tat aaa gat gag gac ctc gac cat 4468
308 Val Trp Cys Gln Lys Arg Ser Asp Tyr Lys Asp Glu Asp Leu Asp His
309          990          995          1000
311 cat cat cat cat cac cgg taataatagg tagataagtg actgattaga 4516
312 His His His His His Arg
313 1005          1010
315 tgcattgac cctcgaccaa ttccggttat ttccaccat attgccgtct tttggcaatg 4576
316 tgaggggeeg gaaacctggc cctgtcttct tgacgagcat tctaggggt ctttcccctc 4636
317 tcgccaaagg aatgcaagg ctgttgaatg tcgtgaagga agcagttcct ctggaagctt 4696
318 cttgaagaca aacaacgtct gtagcgaccc ttgacaggca gcggaacccc ccacctggcg 4756
319 acaggtgcct ctgcggccaa aagccacgtg tataagatac acctgcaaag gcggcacaac 4816

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VERIFICATION SUMMARY

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L:13 M:270 C: Current Application Number differs, Replaced Current Application Number